

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:08:31 ; Search time 17398.4 seconds
(without alignments)
695.856 Million cell updates/sec

Title: US-09-303-518D-569

Perfect score: 897

Sequence: 1 atgttcgttaccatccag.....accgcacaaatgcgcgtaa 897

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues 27472414

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vitc:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.4	4.5	1101	12 CNSO0RK2	AL077673 Drosophl1
2	40	4.5	1009	10 BG701305	BG701305 602682983
3	38	4.2	703	10 B1917026	B1917026 603181414
4	38	4.2	1101	9 AL513871	AL513871 AL513871
5	37.6	4.2	1592	10 BM451350	BM451350 AGENCOURT
6	37.4	4.2	1815	11 AK014308	AK014308 Mus muscu
7	37.2	4.1	972	12 CNSO02JV	AL097765 Drosophl1
8	37	4.1	656	9 AV402539	AV402539 AV402539
9	37	4.1	732	9 AU006052	AU006052 AU006052
10	37	4.1	928	9 BE214094	BE214094 HY_CED000
11	37	4.1	1013	12 CNSO16KT	AL106871 Drosophl1
12	36.4	4.1	884	12 CNSO06U0	AL065923 Drosophl1
13	36.2	4.0	643	9 BB657008	BB657008 BB657008
14	36.2	4.0	643	9 BB657008	BB657008 BB657008
15	36.2	4.0	653	10 BM491204	BM491204 PGP2n-PK0
16	36.2	4.0	685	9 BB645508	BB645508 BB645508
17	36.2	4.0	1012	10 BG115639	BG115639 602316767

C 18	36	4.0	614	12 AQ082014	AQ082014 RPI11-54
C 19	36	4.0	686	10 BG107224	BG107224 602290957
C 20	36	4.0	970	10 BM461835	BM461835 AGENCOURT
C 21	36	4.0	1243	10 BM460646	BM460646 AGENCOURT
C 22	36	4.0	1247	10 BM466205	BM466205 AGENCOURT
C 23	35.8	4.0	343	9 AV673531	AV673531 AV673531
C 24	35.8	4.0	430	10 BG047727	BG047727 OVI_27-A1
C 25	35.8	4.0	507	10 BE599418	BE599418 P11_87_C1
C 26	35.8	4.0	608	9 AV902676	AV902676 AV902676
C 27	35.8	4.0	914	12 CNSO06CP	AL059740 Drosophl1
C 28	35.8	4.0	1201	12 CNSO016N	AL106361 Drosophl1
C 29	35.8	4.0	1990	10 BE965923	BE965923 601659233
C 30	35.6	4.0	563	10 B1975996	B1975996 484611 MA
C 31	35.6	4.0	880	9 AL551924	AL551924 AL551924
C 32	35.4	3.9	330	9 AL1933541	AL1933541 wt40c01.x
C 33	35.4	3.9	695	10 BF622032	BF622032 HVSMEM000
C 34	35.2	3.9	568	10 BF079098	BF079098 229628 MA
C 35	35.2	3.9	700	9 AL502466	AL502466 AV931238
C 36	35	3.9	600	9 AV931238	AV931238 AV931238
C 37	35	3.9	618	10 BM486648	BM486648 PGM2n-PK0
C 38	35	3.9	645	9 AV926352	AV926352 AV926352
C 39	35	3.9	822	10 BG365381	BG365381 HVSMEM1000
C 40	35	3.9	894	10 BM047100	BM047100 603627433
C 41	34.8	3.9	516	9 AV869097	AV869097 AV869097
C 42	34.8	3.9	565	9 AL514205	AL514205 AL514205
C 43	34.8	3.9	840	9 AL530594	AL530594 AL530594
C 44	34.6	3.9	461	9 AW659434	AW659434 96602 MAR
C 45	34.6	3.9	530	9 AW922863	AW922863 DGI_47_H1
C 46	34.6	3.9	548	10 BG560454	BG560454 RH122_74
C 47	34.6	3.9	707	9 AW054381	AW054381 L30-1719Q
C 48	34.6	3.9	869	12 BH132869	BH132869 ENTOLO85TE
C 49	34.6	3.9	910	12 CNSO06ON	AL106362 Drosophl1
C 50	34.6	3.9	1101	12 CNSO14PA	AL104440 Drosophl1
C 51	34.4	3.8	482	10 C06823	C06823 C06823 Rat
C 52	34.4	3.8	512	12 P191L	AL161299 Leishmani
C 53	34.4	3.8	559	12 AQ491449	AQ491449 RPCI_11-2
C 54	34.4	3.8	839	12 CNSO04NB	AL054280 Drosophl1
C 55	34.4	3.8	1101	12 CNSO17SY	AL108460 Drosophl1
C 56	34.2	3.8	627	9 A1825645	A1825645 wb75b05.x
C 57	34.2	3.8	629	9 AV872025	AV872025 AV872025
C 58	34.2	3.8	730	9 BB645299	BB645299 BB645299
C 59	34.2	3.8	909	12 CNSO0JTL	AL076720 Drosophl1
C 60	34.2	3.8	1100	12 CNSO16KD	AL106655 Drosophl1
C 61	34.2	3.8	407	10 BF039324	BF039324 BP25009A
C 62	34	3.8	491	10 BE776714	BE776714 MY-19-E-0
C 63	34	3.8	588	9 AL552306	AL552306 AL552306
C 64	34	3.8	612	9 AW587084	AW587084 EST138707
C 65	34	3.8	658	12 AQ397507	AQ397507 mxb00093
C 66	34	3.8	765	10 BG584885	BG584885 EST486646
C 67	34	3.8	802	10 BE368219	BE368219 601222141
C 68	34	3.8	1194	10 BG820654	BG820654 602782958
C 69	33.8	3.8	425	12 AZ048716	AZ048716 GSSBRU010
C 70	33.8	3.8	455	10 BE773885	BE773885 283396 MA
C 71	33.8	3.8	455	10 W07842	W07842 zb04b03.r1
C 72	33.8	3.8	478	10 BM286331	BM286331 526343 MA
C 73	33.8	3.8	480	10 BM258834	BM258834 523748 MA
C 74	33.8	3.8	508	10 BM114584	BM114584 LO807B07
C 75	33.8	3.8	525	9 AW219511	AW219511
C 76	33.8	3.8	645	12 CNSO1213	AL101589 Drosophl1
C 77	33.8	3.8	727	12 B1805731	B1805731 S043412.S
C 78	33.8	3.8	895	12 CNSO071A	AL066286 Drosophl1
C 79	33.6	3.7	287	9 AV131659	AV131659 AV131659
C 80	33.6	3.7	360	10 C42003	C42003 C42003 Yuj1
C 81	33.6	3.7	367	10 B1720178	B1720178 1031048B0
C 82	33.6	3.7	471	9 AV624652	AV624652 AV624652
C 83	33.6	3.7	487	9 A1336998	AL1336998 qx87e10.x
C 84	33.6	3.7	487	10 B1183298	B1183298 UNL-P-FN-
C 85	33.6	3.7	489	10 B1186294	B1186294 UNL-P-FN-
C 86	33.6	3.7	498	9 AW594194	AW594194 h962a01.x
C 87	33.6	3.7	517	10 B1874475	B1874475 963115H01
C 88	33.6	3.7	546	9 AM237064	AM237064 xms2902.x
C 89	33.6	3.7	551	9 A1989498	A1989498 ws25e01.x
C 90	33.6	3.7	588	10 BE463918	BE463918 hy18h06.x

C	91	33.6	3.7	601	10	B1718274	B1718274	1031030F0
	92	33.6	3.7	645	10	BM40578	BM40578	p41n.-PK0
	93	33.6	3.7	725	10	B1517775	B1517775	603042019
C	94	33.6	3.7	735	10	B1993866	B1993866	1031005B0
C	95	33.6	3.7	786	10	BG845957	BG845957	1024011C0
C	96	33.6	3.7	832	9	AL534397	AL534397	AL534397
C	97	33.6	3.7	893	9	AL521848	AL521848	AL521848
C	98	33.6	3.7	937	9	AL534844	AL534844	AL534844
	99	33.6	3.7	968	10	B1225970	B1225970	602955048
	100	33.6	3.7	1101	12	CNS0150D	AL104839	Drosophila

ALIGNMENTS

[illegible]

Qy	588	cctgcgcgaccacggtccctccctcaagaag	619
		:: :::::::::::::: :: ::	
Db	1067	AGKKKKKMMMMKKMMMVNDGKMMMAKMDK	1098

LOCUS	DEFINITION	RESULT 1
CNS00K2		
CNS00K2	1101 bp DNA	linear GSS 03-JUN-1999
CNS00K2	Drosophila melanogaster genome survey sequence T7 end of BAC:	
	BACR17F22 of RPc1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	

ACCESSION	AL017163	GI:4957249
VERSION	AL017163.1	
KEYWORDS	GSS.	
SOURCE	fruit fly.	
ORGANISM	Drosophila melanogaster	

REFERENCE
TITLE
AUTHORS
JOURNAL
Direct Submission
Submitted 02-JUN-1999
Genoscope - Centre National de Sequencage
Paris, FRANCE / E-mail: secref@genoscope.cns.fr

COMMENT

Submitted (2-JUN-1999) Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org/TheBDGP/Drosophila>
melanogaster BAC library was prepared by Kazutoyo Oosagawa and
Aarcen Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPc1-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain v²: cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

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/organism="Drosophila melanogaster"  
/db_xref="taxon:7227"  
/clone_lib="RPCI-98"  
/db_xref="taxon:7227"
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BASE COUNT	191 a	94 c	163 g	151 t	502 others
ORIGIN					

```
Query Match      4.58; Score 40.4; DB 12; Length 1101;
Best Local Similarity 9.6%; Pred. No. 2.5;
Matches 32; Conservative 159; Mismatches 141; Indels 0; Gaps 0.
```

QY 288 agacatagaacaatgttccaagcgtacacgcgtggaacatgttcagcagcgttgg 347

Db 767 AKAGMAMMAAMMAKBDMAKAMMMMMGMMMMVVMGMMGMMGKGHMMGRKMGKTYM 826

QY 348 caaacacgaaagcgctgctatcatcatcaacgcgcacacatcgcgacgctacgatttgggcgagac 407

Db 827 MRKNNVNMGMMAKNNMNBAMMMMMMMKMMNKDKMNNMCITIKCMNMKMYMMMMMMMAK 886

RESULT	2
BC701305/c	
LOCUS	BC701305
DEFINITION	1009 bp mRNA linear EST 07-MAY-2001
	602662933F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:481580 5',
	mRNA sequence.

ACCESSION	BG701305	
VERSION	BG701305.1	GI:13971506
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Ctenulata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1009)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
email.nih.gov

E-mail: cagdas.temel@nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA library preparation: Michael J. Brownstein (NHGR), Shrawan
 Toshilakki and Piero Carninci (NIKE)
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLML0712 row: f column: 21
 High quality sequence stop: 121.
 Location/Qualifiers

FEATURES
source

```

1. 1005
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4815380"
/clone_1ib="NIH_MGC_95"
/tissue_type="hippocampus"

```

BASE COUNT 245 a 243 c 260 g 260 t 1 others

ORIGIN

/140_108c- univec
 /note="Organ: Brain; Vector: pluescript (modified
 pluescript KS+); Site_1: BamHI; Site_2: SalI; xhoI (gtcga
 g); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.5 kb and
 normalized to 10^5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIMH/NHRI, National
 Institutes of Health). Note: this is a NIH-MGC Library.

Query Match	4.5%;	Score 40;	DB 10;	Length 1009;
Best local Similarity	57.0%;	Pred. No. 3.2;		
Matches	73;	Conservative	0;	Mismatches 55; Indels 0; Gaps 0

QY 549 atcatcaagccctgcgttcgagggaagaaccaatcgtcttgcggaccacagtccctc 608
||||| ||| ||||| | | ||| ||| ||| ||| ||| ||| |||
Db 137 AATCAGCAATGCCCTGGGCCCCACGTACGTCCTCCAGCATCCAGCGCACACAAGCACCATT 78


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/clone="320002M13"
/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="14, 17 days embryo"
1..1815
/misc_feature
  /note="data source:SPTR, source key:09NZ65, evidence:ISS
  homolog to ORPHAN G-PROTEIN COUPLD RECEPTOR"
BASE COUNT      342 a      544 c      503 g      426 t
ORIGIN

Query Match      4.2% Score 37.4; DB 11; Length 1815;
Best Local Similarity 49.7%; Pred. No. 22;
Matches 95; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 433 ccgcgcacgcacatgacaaacccgcgaataaagatagacaaatcatgcaagc 492
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1162 CCGCGACACAGCGTGTACACGCCACCGAGATGGCCCTGATGACCAAGGCCGCTGAA 1221
QY 493 ggcaggggttcgcgcgaagaacacccgcctaccagacatacaagggtcaacaatc 552
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1222 GGTGCATACGACGTCTCCACAGGCGCACCGCAACAGCAGGTATGGCAGTGC 1281
QY 553 atcaagccctgcgttcgcgcgaagaacacatgctctgcgccgccacgtccctccct 612
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1282 AACTCAACCTCGCGGCGGCGAAGACATGATGTCAGACCCACAGGTGGCCACGCCA 1341
QY 613 caagaagcgcg 623
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1342 CCAAAAGACGG 1352

RESULT 7
CNS002JY/c 972 bp DNA linear GSS 26-JUL-1999
LOCUS      Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN02G13 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AF097765
VERSION     AF097765.1 GI:5609376
KEYWORDS   GSS.
SOURCE      fruit fly.
            Drosophila melanogaster
ORGANISM   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 972)
AUTHORS    Genoscope.
TITLE      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL    BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billard at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBelobAC11.

FEATURES
  source      1..972
              Location/Qualifiers
                /organism="Drosophila melanogaster"
                /plasmid="pBelobAC11"
                /db_xref="taxon:7227"
                /clone_lib="DrosBAC"
                /clone="BACN02G13"
                /note="end : 77"
                /dev_stage="spinning stage day-3"

BASE COUNT    293 a      111 c      92 g      111 t      365 others
ORIGIN

Query Match      4.1% Score 37.2; DB 12; Length 972;

/clone="320002M13"
/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="14, 17 days embryo"
1..1815
/misc_feature
  /note="data source:SPTR, source key:09NZ65, evidence:ISS
  homolog to ORPHAN G-PROTEIN COUPLD RECEPTOR"
BASE COUNT      342 a      544 c      503 g      426 t
ORIGIN

Query Match      4.1% Score 37; DB 9; Length 656;
Best Local Similarity 51.5%; Pred. No. 18;
Matches 85; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 286 gaagacataagaagaacatggttaagcggtacagcggtgggaacatgtgcagcagcgttg 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 72 GAACAACCTAGAGATGGGCTCCAGAACACCGTGTAGTAGAGAGAACATTCCCAAGCGCTCG 131
QY 346 gacaaacacgaagggcgtgcattcatcacgcgcgcacacatgcagcagcgttcgttgaggga 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 132 GACGCTCTCTGACGCGGCTCTCCAGAACACTGCAGAGAGAGAGTGCATGCTGTGTGAC 191

Best Local Similarity 21.2%; Pred. No. 19;
Matches 43; Conservative 79; Mismatches 81; Indels 0; Gaps 0;

QY 157 gacgcgcgcgcacatcgcgcacatattgcctcagcagcagcagcagcagcagcagcagcagc 216
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
DB 866 RMMAMKDDANAMRRKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMM 807
QY 217 gtcaaacgcgttttcggaacgcgcgaacgaagcggtttggaacttgccccgcgttttc 276
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
DB 806 RKRTRDCACRRKKKKKKKTTMMAMMMAMMMKGGGGGGGRRAMKMKKKTKTTAAAR 747
QY 277 agaaacacggaagacataagaacaatgttcaagcggtacacgagcgttggaacatgtgcag 336
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
DB 746 TAAAMGTGGAAMARMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMM 687
QY 337 cagcgtttggaacacacgaag 359
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
DB 686 AMGRKARTRAMAMAMKMAKRR 664

RESULT 8
AV402539      656 bp mRNA linear EST 05-FEB-2000
LOCUS      AV402539 Bombyx mori C108 spinning stage day-3 Bombyx mori cDNA
DEFINITION Clone hes30094 T3, mRNA sequence.
ACCESSION  AV402539
VERSION     AV402539.1 GI:6906191
KEYWORDS   EST.
SOURCE      domestic silkworm.
ORGANISM   Bombyx mori
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylsia
            1 (bases 1 to 656)
            Mita,K., Moriyama,M., Shimada,T., Okano,K. and Maeda,S.
            Bombyx mori cDNA
            Unpublished (2000)
            Contact: Mita K
            Genome Research Group
            National Institute of Radiological Sciences
            Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
            Email: kmita@nirs.go.jp
            method:uni-directional, sequence direction:sequenced from T3 primer
            (5' -> 3')
            Project="Silkworm Genome Program in MAFF, and Research for the
            Future Program in JSPS, see 'Silkbase',
            <http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES
  source      1..656
              Location/Qualifiers
                /organism="Bombyx mori"
                /strain="C108"
                /db_xref="taxon:7091"
                /clone="hes30094"
                /clone_lib="Bombyx mori C108 spinning stage day-3"
                /sex="female/male mixed"
                /cell_type="hemocyte"
                /dev_stage="spinning stage day-3"

BASE COUNT    185 a      178 c      165 g      127 t      1 others
ORIGIN

Query Match      4.1% Score 37; DB 9; Length 656;
Best Local Similarity 51.5%; Pred. No. 18;
Matches 85; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 286 gaagacataagaagaacatggttaagcggtacagcggtgggaacatgtgcagcagcgttg 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 72 GAACAACCTAGAGATGGGCTCCAGAACACCGTGTAGTAGAGAGAACATTCCCAAGCGCTCG 131
QY 346 gacaaacacgaagggcgtgcattcatcacgcgcgcacacatgcagcagcgttcgttgaggga 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 132 GACGCTCTCTGACGCGGCTCTCCAGAACACTGCAGAGAGAGAGTGCATGCTGTGTGAC 191
```

OY	406	cgcgaactcagccaggcttcggtccgccgtacacggcatgtac	450
Db	192	ACGACTCGAGTCACTCCTCGTCGAGATCCTGTGGCCGACATGAAC	236
<hr/>			
RESULT 9			
LOCUS	AU006052	732 bp	mRNA EST 19-JAN-1999
DEFINITION	AU006052 Bombyx mori p50(Dalzo) Bombyx mori cDNA clone wv40412,		
ACCESSION	mRNA sequence.		
VERSION	AU006052		
KEYWORDS	AU006052.1 GI:4163436		
SOURCE	EST.		
ORGANISM	domestic silkworm.		
	Bombyx mori		
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dltysia		
	; Bombycoidea; Bombycidae; Bombyx.		
REFERENCE	1 (bases 1 to 732)		
AUTHORS	Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.		
TITLE	Establishment of cDNA database of Bombyx mori		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Mita K Genome Research Group National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmite@nirs.go.jp PROJECT = 'CREST project by JST'. Location/Qualifiers		
FEATURES			
source	1..732 /organism="Bombyx mori" /strain="p50(Dalzo)" /db_xref="taxon:7091" /clone="wv40412" /clone_lib="Bombyx mori p50(Dalzo)"		
BASE COUNT	180 a 214 c 198 g 140 t		
ORIGIN			
<hr/>			
Query Match	4.1%:	Score 37;	DB 9; Length 732;
Best Local Similarity	51.5%;	Pred. No. 19;	
Matches	85;	Conservative	0; Mismatches 80; Indels 0; Gaps 0;
OY	286	gaagaacatgaacaactgttcaagaagcytaacagcgctggaaacatgtcagcagcgttg	345
Db	340	GAAACAACACTGAATTCGGTGCTCAAGAACAACCTAATTAGAGAAACATTCGCAGAGCTCTG	399
OY	346	gacaaacagaaagcgctttattcatcacccgcacatatcgscagtacgatlttgagcgga	405
Db	400	GACGGCTCTGCACGGGCTCTCCAGAAACTGCAGAGCGAGTCATCATCTTGTGAC	459
OY	406	cgcatacatcagccagcagcttcggtccgcgcgcagcgcgatgtac	450
Db	460	ACGTAAGTAGTACCTCGTCGAGATGTGTGGCCGACATGAAC	504
<hr/>			
RESULT 10			
LOCUS	BE214094	928 bp	mRNA linear EST 23-OCT-2001
DEFINITION	HV.CEB0002D12f Hordeum vulgare seedling green leaf EST library		
ACCESSION	HVCNDA0005 (Blumeria challenged) Hordeum vulgare cDNA clone		
VERSION	HV.CEB0002D12f.mRNA sequence.		
KEYWORDS	BE214094		
SOURCE	BE214094.1 GI:8901706		
ORGANISM	barley.		
	Hordeum vulgare		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae		
	; Triticeae; Hordeum.		
REFERENCE	1 (bases 1 to 928)		
AUTHORS	Wing,R., Close,T.J., Kleinhoofs,A., Wise,R., Wel,F., Begun,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi		

TITLE	D.W., Fenton, R.D., Gates, R. and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mia6) seedling leaf cDNA library			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total hg bases = 450 Seq primer: AATTACCTCCTCAAGGC High quality sequence stop: 570.			
FEATURES	location/Qualifiers			
source	1..928 /organism="Hordeum vulgare" /cultivar="C116151 (Mia6)" /db_xref="taxon:4513" /clone="HV_CEB0002D12f" /clone_id="Hordeum vulgare seedling green leaf EST library HVCDNA0005 (Blumeria challenged)" /issue_type="seedling green leaf" /lab_host="SOLR" /note="Vector: lambdaZAP; Site:1: EcoRI; Site:2: XhoI; C.I. 16151 (Mia6) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate 5674 (AvrMia6 of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the T1 Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates Rando, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders see Close '00, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genomics Newsletter 31:29-30. (http://wheat.pw.usda.gov/g9pages/D9n/31/clover.html)"			
BASE COUNT	159 a 319 c 308 g 138 t 4 others			
ORIGIN				
Query Match	4.1%; Score 37; DB 9; Length 928;			
Best Local Similarity	56.0%; Pzed. No. 21;			
Matches	70; Conservative 0; Mismatches 55; Indels 0; Gaps 0			
QY	333	gcagcagcgtttggacaacagaagagcgtgcgtatcatcatcagccgacatcgcagcagcta	392	
DB	249	gctggcgccccagagacacacagagcgcaggttcgcaattgcgccttgagacgcggcattccc	308	
QY	393	cgatttggcgcagcgtacatcagcagcagcgttccttcctgcgtcagcgcagcgtatgata	452	
DB	309	ggcattcctctggcattatctccacgcagcgccttggccattccgtccatgacat	368	
QY	453	accgc 457		
DB	369	ggcgc 373		

RESULT 11
 CDS016KT
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence SP6 end of BAC
 BACN16116 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION
 AL106871
 VERSION
 AL106871.1 GI:5624218
 KEYWORDS
 GSS.
 SOURCE
 fruit fly.
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE
 1 (bases 1 to 1013)
 Genoscope.
 AUTHORS
 TITLE
 JOURNAL
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr)
 COMMENT
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelosBAC11.
 FEATURES
 source
 1..1013
 /organism="Drosophila melanogaster"
 /plasmid="pBelosBAC11"
 /db_xref="taxon:7227"
 /clone_lib="DrosBAC"
 /clone="BACN16116"
 /note="end : SP6"
 BASE COUNT 132 a 191 c 148 g 131 t 411 others
 ORIGIN

Query Match 4.1%; Score 37; DB 12; Length 1013;
 Best Local Similarity 15.6%; Pred. No. 22;
 Matches 41; Conservative 92; Mismatches 130; Indels 0; Gaps 0;

QY 370 atcaagccgacatcgcaagctacgattgagcgagctacacgacgagcttcg 429
 Db 200 MTKMCMNATATCCCMNMCCCTGTNNMMNMCNMCNMCNMCNMCNMCNMCN 259
 QY 430 ttccgctgacgcatgataaacgagcaaacatcaagcagatagcaaacatgacg 489
 Db 260 MYSCSCCCMGMNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMC 319
 QY 490 gcgagcgaggttcgagcaagaaacgagcctacgacatacagaggtcaacaa 549
 Db 320 TTHMMNMTTNNMGNNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNG 379
 QY 550 atcaacagcctgctgagcgagcaagcaccatgctcgcgacacgctccctcc 609
 Db 380 NTCTTGAGMCMNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMC 439
 QY 610 cctcaagaagcgaggaagcgt 632
 Db 440 MNNMCMNMMNMMNMGNGNNGMNT 462

RESULT 12
 CDS006U/c
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence T7 end of BAC #
 BACR14N21 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION
 AL065923

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE
 1 (bases 1 to 884)
 Genoscope.
 AUTHORS
 TITLE
 JOURNAL
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr)
 COMMENT
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoler in Peter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp. the same strain used for the BDGP's
 pi and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 FEATURES
 source
 1..884
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR14N21"
 /note="end : T7"
 BASE COUNT 230 a 62 c 139 g 124 t 329 others
 ORIGIN

Query Match 4.1%; Score 36.4; DB 12; Length 884;
 Best Local Similarity 15.0%; Pred. No. 31;
 Matches 32; Conservative 95; Mismatches 87; Indels 0; Gaps 0;

QY 405 agctacatcagcagcagcttcgctccgctgacgcatgataaacgagcaaat 464
 Db 857 KMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMM 798
 QY 465 caaagcgatagcaaatatcgagcgaggttcgagcagcaagaaacgagcc 524
 Db 797 KMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMM 738
 QY 525 tacggacatacgaaggggttaaacatcaaacgctcgttcgagcagacacat 584
 Db 737 KMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMMNMM 678
 QY 585 cgtcctgcgagcagcagctccctccctcaagaa 618
 Db 677 MCCACMCCAMACCMNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMCNMC 644

RESULT 13
 BB620231/c
 LOCUS
 DEFINITION
 BB620231 RIKEN full-length enriched, adult male thymus Mus musculus
 cDNA clone 5832421E21 5', mRNA sequence.
 ACCESSION
 BB620231
 VERSION
 BB620231.1 GI:16459352
 KEYWORDS
 EST.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 643)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 970)
NIH-MGC <http://mhc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12219 row: h column: 17
High quality sequence stop: 506.
Location/Qualifiers
1. 970
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:553388"
/clone_lib="NIH-MGC-71"
/issue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 181 a 307 c 302 g 179 t 1 others
ORIGIN
Query Match 4.0%; Score 36; DB 10; Length 970;
Best Local Similarity 46.4%; Pred. No. 42;
Matches 117; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
QY 310 gcggtacacgctggaacatgtcagcaagctttgacaacaacaggaaggtctatc 369
DB 157 GCGTTGCTGGGCTGGGCGGCGGACAGCCGCCGCCCGCCGACCGGGGCTGGATTG 216
QY 370 atcacgcgcacatgcagctacgattggcgagcgtatcacagccagctccg 429
DB 217 GCCGCCCGCGCCACTACAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 276
QY 430 ttccgcgtacgcgcattgacaaacccgcgaataacacgcatagacaataatcatgag 489
DB 277 AAGATGTGAGAGGCTTTTGTGATCGCGCGCCAGCATCTGTGAGGACAACTGTGGAG 336
QY 490 gcgggacaggttcgcggagaaagaaacgcgcctaccagcatagaggggtcaaaaca 549
DB 337 GACCTGAGAGCGCGGAGAGGAGAGGAGCAAGGAGCGGCGGCGGCGGCGGCGGCGG 396
QY 550 atcatcaagcc 561
DB 397 ATCATCAAGCCC 408
RESULT 21
BM460646 1243 bp mRNA linear EST 05-FEB-2002
LOCUS BM460646
DEFINITION AGENCOURT_6421419 NIH-MGC_71 Homo sapiens CDNA clone IMAGE:5531991
5', mRNA sequence.
ACCESSION BM460646
VERSION BM460646.1 GI:18509686
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1243)
NIH-MGC <http://mhc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12214 row: i column: 16
High quality sequence stop: 439.
Location/Qualifiers
1. 1243
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5531991"
/clone_lib="NIH-MGC-71"
/issue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SF0RT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 172 a 553 c 260 g 258 t
ORIGIN
Query Match 4.0%; Score 36; DB 10; Length 1243;
Best Local Similarity 46.4%; Pred. No. 46;
Matches 117; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
QY 310 gcggtacacgctggaacatgtcagcaagctttgacaacaacaggaaggtctatc 369
DB 181 GCGTTGCTGGGCTGGGCGGCGGACAGCCGCCGCCCGCCGACCGGGGCTGGATTG 240
QY 370 atcacgcgcacatgcagctacgattggcgagcgtatcacagccagctccg 429
DB 241 GCCGCCCGCGCCACTACAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 430 ttccgcgtacgcgcattgacaaacccgcgaataacacgcatagacaataatcatgag 489
DB 301 AAGATGTGAGAGGCTTTTGTGATCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 490 gcgggacaggttcgcggagaaagaaacgcgcctaccagcatagaggggtcaaaaca 549
DB 361 GACCTGAGAGCGCGGAGAGGAGAGGAGCAAGGAGCGGCGGCGGCGGCGGCGGCGG 420
QY 550 atcatcaagcc 561
DB 421 ATCATCAAGCCC 432
RESULT 22
BM466205 1247 bp mRNA linear EST 05-FEB-2002
LOCUS BM466205
DEFINITION AGENCOURT_6457149 NIH-MGC_92 Homo sapiens CDNA clone IMAGE:5576950
5', mRNA sequence.
ACCESSION BM466205
VERSION BM466205.1 GI:18515247
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1247)
NIH-MGC <http://mhc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

QY 397 ttggcgagcgcctacatcagccagcagcttcglt 431
 1 || ||||| | ||| ||
 Db 461 CGACTACTCCTTCATCAGTACATTCTGAAT 495

RESULT	27
CNS00CAP/c	CNS00CAP/c
LOCUS	CNS00CAP 914 bp DNA linear GSS 04-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence 17 end of BAC #
ACCESSION	BACR6P05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
	AI059740

FEATURES	source	location/qualifiers
	1..914	
	/organism="Drosophila melanogaster"	
	/db_xref="taxon:7227"	
	/clone_id="RPC1-98"	
	/clone="BACR26P05"	
	/note="end : 77"	
BASE COUNT	146 a	173 t 361 others
ORIGIN	121 c	113 g

RESULT	28
CNS0166N/C	
LOCUS	CNS0166N
DEFINITION	1201 bp DNA linear GSS 26-JUL-1999
ACCESSION	Drosophila melanogaster genome survey sequence T7 end of BAC BA0N15422 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence. AI106361

COMMENT

Immortalization of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.dbi.ac.uk>. This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

LOCUS BE965323 1990 bp mRNA linear EST 14-DEC-2000
DEFINITION B01659233R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895593 3',
mRNA sequence.
ACCESSION BE965323
VERSION BE965323.2 GI:11769567
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

/tissue_type="Seedling shoot"
/lab_host="TJ0121"

Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 50C for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give phagescript SK(-) cDNA phagemids. These steps were performed in the TJ Close Laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html>)

BASE COUNT
ORIGIN

130 a 229 c 230 g 105 t 1 others

Query Match
Best Local Similarity 55.2%; Score 35.4; DB 10; Length 695;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 333 gcaagcagcttgacaaacaggaagcgtctatcattacagccagacatcgagcgtca 392
DB 90 gctggccgccgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 149
QY 393 cgattggcgagcgtacatcagcagcagcgttcgcttcgcttcgagccagcgtca 452
DB 150 gggcattcctcgacatcctccacgacgacgacgacgacgacgacgacgacgacgac 209
QY 453 accgc 457
DB 210 ggcgc 214

RESULT 34
BF079098 568 bp mRNA linear EST 18-OCT-2000
LOCUS
DEFINITION 229628 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF079098
VERSION BF079098.1 GI:10872928
KEYWORDS
SOURCE EST.
ORGANISM Sus scrofa
Pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 568)
Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keeler, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov

FEATURES
SOURCE

Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
REVERSE: GTTTCCTCCAGTCAGCAGC
plate: 45 row: J column: 3
Seq primer: ATTGCTGACACTATAG.
Location/Qualifiers
1..568
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_1lb="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT
ORIGIN

104 a 170 c 182 g 111 t 1 others

Query Match
Best Local Similarity 48.5%; Score 35.2; DB 10; Length 568;
Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 164 cgcgcatcgtcgcaatctgctgcagcagcagcagcagcagcagcagcagcagcagc 223
DB 438 cccacacgcttcacatccctcctcagcagcagcagcagcagcagcagcagcagcagc 379
QY 224 ccgcttctggcgaacagcgaacagcagcagcagcagcagcagcagcagcagcagc 283
DB 378 aagttgctgcgcgcac 319
QY 284 cgaagacatagaaacatgctcaagcagcagcagcagcagcagcagcagcagcagc 343
DB 318 atgtccacatgtagacatcctcctcctcagcagcagcagcagcagcagcagcagc 259
QY 344 tggacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 363
DB 258 tcggagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 239

RESULT 35
AL502466 700 bp mRNA linear EST 04-JAN-2001
LOCUS
DEFINITION AL502466 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone
ACCESSION HM07K20u 3', mRNA sequence.
VERSION AL502466
KEYWORDS
SOURCE EST.
ORGANISM Hordeum vulgare
Barley.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 700)
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, <http://pgrc.ipk-gatersleben.de>
Seq primer: M13uni primer for 3' end.
Location/Qualifiers
1..700
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone_1lb="HM07K20u"
/tissue_type="roots"

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 565)	Li, W. B., Gruber, C., Jeessee, J. and Polayes, D.	Full-length cDNA libraries and normalization	unpublished (2001)	Genoscope : Centre National de Séquençage

FEATURES	Location/Qualifiers
COURSE	1 565

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBB0062612"
/clone_1fb="T11_NFL006_P12"
/tissue_type="Placenta"
/vector="pCMWSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
Eco RV sites of the pCMWSPORT 6
cloned into the Not I and Eco RV sites of the pCMWSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng liang Life Technologies
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

```

```

/db_xref="taxon:9606"
/clone="CS0DD008YD01"
/clone_lib="LFI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
was enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technology, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA fax :
(1) 301 610
8371 Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"
129 a 284 c 278 g 144 t 5 others

```

Query Match	3.9%;	Score 34.8;	DB 9;	Length 840;
Best Local Similarity	52.1%;	Pred. No. 85;		
Matches	75;	Mismatches	68;	Indels 0;
		Gaps		0;

Accession	Sequence	Position
QY	562 ctgcgtcttgaggcgaaagacacatgctctgccgcagacaagctccctccccaagaagc	6
Db	156 ttggggccggcgtccacacacatagtgtccgcccaactgacccccctcccgagaaagcc	97
QY	622 ggggaagcgtatggctgattcttcgcgaacactgtgctataccatgacgttgcgcga	68
Db	96 gggggcggcgagggggccgcccacccggggagcccgccagggcggaagggaacg	37
QY	682 aaattgycacacgttcaagcgtg	705
Db	36 aaaccctgctagtggaagtgagg	13

RESULT	44			EST 25-APR-2003
AM659434/C		481 bp	mRNA	
LOCUS			linear	
DEFINITION	96602 MARC	IBOV Bos	taurus	CDNA sequence.
ACCESSION	AM659434			
VERSION	AM659434.1	GI:7425261		
KEYWORDS	EST.			
SOURCE				
ORGANISM	Cow, +taurus			

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
1 (bases 1 to 488)	Smith, T.P.L., Grosbe, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casae, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pariza, G., Holt, I., Karamycheva, S., Hwang, F., Quackenbush, J. and Keefe, J.W.	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	Genome Res. 11 (4), 626-630 (2001)		Contact: Smith TPL National Research Center

RESULT 43	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
AL530594/C	AL530594	AL530594.L1.NF.L001.NBC4	AL530594	AL530594	EST.	human.	Homo sapiens	1 (bases 1 to 840)	Li, W. B., Gruber, C., Jessee, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope	BP 191 91006 EVRY cedex - France
		prime, mRNA sequence.	840 bp										Email: secref@genoscope.cns.fr , Web : www.genoscope.cns.fr .
													location/Qualifiers
													1..840
													/organism="Homo sapiens"

